



**Exhibit A**  
**C mparison SEQ ID NO:4 vs. IPI00044749.2**

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAAxJayWj: 1214 aa

>seqid4

vs /tmp/fastaDAAYJayWj library

searching /tmp/fastaDAAYJayWj library

1258 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized; BL50 matrix (15:-5)] ktup: 2

join: 40, opt: 28, gap-pen: -12/ -2, width: 16

Scan time: 0.066

The best scores are:

opt

IPI00044749.2

(1258) 4775

>>IPI00044749.2

(1258 aa)

initn: 4773 initl: 4773 opt: 4775

Smith-Waterman score: 7822; 96.343% identity in 1258 aa overlap (1-1214:1-1258)

	10	20	30	40	50	60
seqid4	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH					
	.....					
IPI000	MEKYVRLQKIGEGSFGKAILVKSTEDGRQYVIKEINISRMSSKEREESRREVAVLANMKH					
	10	20	30	40	50	60
	70	80	90	100	110	120
seqid4	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVH					
	.....					
IPI000	PNIVQYRESFEENGSLYIVMDYCEGGDLFKRINAQKGVLFQEDQILDWVQICLALKHVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
seqid4	DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
	.....					
IPI000	DRKILHRDIKSQNIFLTKDGTVQLGDFGIARVLNSTVELARTCIGTPPYLSPEICENKPY					
	130	140	150	160	170	180
	190	200	210	220	230	240
seqid4	NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIIISGSFPPVSLHYSYDLRSLVSQLFK					
	.....					
IPI000	NNKSDIWALGCVLYELCTLKHAFEAGSMKNLVLKIIISGSFPPVSLHYSYDLRSLVSQLFK					
	190	200	210	220	230	240
	250	260	270	280	290	300
seqid4	RNPRDRPSVNSILEKGFIKRIEFLSPQLIAEEFCLKTFSKFGSQPIPAKRPAŠGQNSI					
	.....					
IPI000	RNPRDRPSVNSILEKGFIKRIEFLSPQLIAEEFCLKTFSKFGSQPIPAKRPAŠGQNSI					
	250	260	270	280	290	300
	310	320	330	340	350	360
seqid4	SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPEKRVNTGEERRKISE					

```

IPI000 SVMPAQKITKPAAKYGIPLAYKKYGDKKLHEKKPLQKHQAHQTPEKRVNTGEERRKISE
      310      320      330      340      350      360
seqid4      370      380      390      400      410      420
EAARKRRLEFIEKEKKQKDQIIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
IPI000 EAARKRRLEFIEKEKKQKDQIIISLMKAEQMKRQEKERLERINRAREQGWRNVLSAGGSGE
      370      380      390      400      410      420
seqid4      430      440      450      460      470
VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPER---
IPI000 VKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQMQQQRAEDNEAKWKREIYGRGLPERGIL
      430      440      450      460      470      480
seqid4 -----480      490
-----QKGQLAVERAKQVEEFLQR
IPI000 PGVRPGFPYGAAGHHFPDADDIRKTLKRLKAVSKQANANRQKGQLAVERAKQVEEFLQR
      490      500      510      520      530      540
seqid4      500      510      520      530      540      550
KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKKEANHSEGQEGSSEADM
IPI000 KREAMQNKARAEGHMVYLARLRQIRLQNFNERQQIKAKLRGEKKKEANHSEGQEGSSEADM
      550      560      570      580      590      600
seqid4      560      570      580      590      600      610
RRKKIESLKAHANARA AVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
IPI000 RRKKIESLKAHANARA AVLKEQLERKRKEAYEREKKVWEEHLVAKGVKSSDVSPPLGQHE
      610      620      630      640      650      660
seqid4      620      630      640      650      660      670
TGGSPSKQQMRSVISVTSALKEVGVDSSTLDTRETSEEMQKTNNAISSKREILRRLNENL
IPI000 TGGSPSKQQMRSVISVTSALKEVGVDSSTLDTRETSEEMQKTNNAISSKREILRRLNENL
      670      680      690      700      710      720
seqid4      680      690      700      710      720      730
KAQEDEKGMQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGQLVIPLDELTLDTSF
IPI000 KAEDEKGMQNLSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGQLVIPLDELTLDTSF
      730      740      750      760      770      780
seqid4      740      750      760      770      780      790
TTERHTVGEVIKLGPNNGSPRRWGKSPTDSVLKILGEAELQLQTELENTTIRSEISPEG
IPI000 TTERHTVGEVIKLGPNNGSPRRWGKSPTDSVLKILGEAELQLQTELENTTIRSEISPEG
      790      800      810      820      830      840
seqid4      800      810      820      830      840      850
EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
IPI000 EKYKPLITGEKKVQCISHEINPSAIVDSPVETKSPEFSEASPQMSLKLEGNLEEPDDLET
      850      860      870      880      890      900
seqid4      860      870      880      890      900      910
EILQEPSGTNKDES L PCTITDVWISSEKETKETQSADRITIQENEVSEDGVSSSTVDQLSD

```

```

IPI000 EILQEPSGTNKNDESLPCTITDVWISSEKETKETQSADRITIQENEVSEDGVSSTVDQLSD
          910          920          930          940          950          960

          920          930          940          950          960          970
seqid4 IHIEPGTND SQH SKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
:.....
IPI000 IHIEPGTND SQH SKCDVDKSVQPEPFFHKVVHSEHLNLVPQVQSVQCSPEESFAFRSHSH
          970          980          990          1000          1010          1020

          980          990          1000          1010          1020          1030
seqid4 LPPKNKNKNSLLIGLSTGLFDANNPKMLR TC SLPDLSKLFRTLMDVPTVGDV RQDNLEID
:.....
IPI000 LPPKNKNKNSLLIGLSTGLFDANNPKMLR TC SLPDLSKLFRTLMDVPTVGDV RQDNLEID
          1030          1040          1050          1060          1070          1080

          1040          1050          1060          1070          1080          1090
seqid4 EIKDENIKEGPSDSEDIVFEETD TDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
:.....
IPI000 EIEDENIKEGPSDSEDIVFEETD TDLQELQASMEQLLREQPGEEYSEEEESVLKNSDVEP
          1090          1100          1110          1120          1130          1140

          1100          1110          1120          1130          1140          1150
seqid4 TANGTDVADEDDNPSSSESALNEEWHS D NSDGEIASECECD SVFNHLEELRLHLEQEMGFE
:.....
IPI000 TANGTDVADEDDNPSSSESALNEEWHS D NSDGEIASECECD SVFNHLEELRLHLEQEMGFE
          1150          1160          1170          1180          1190          1200

          1160          1170          1180          1190          1200          1210
seqid4 KFFEVEY E K I K A I H E D E N I E I C S K I V Q N I L G N E H Q H L Y A K I L H L V M A D G A Y Q E D N D E
:.....
IPI000 KFFEVEY E K I K A I H E D E N I E I C S K I V Q N I L G N E H Q H L Y A K I L H L V M A D G A Y Q E D N D E
          1210          1220          1230          1240          1250

```